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PCT09

RAW SEQUENCE LISTING

DATE: 10/11/2001

PATENT APPLICATION: US/09/807,470

TIME: 10:54:43

Input Set : A:\0020-4850P.ST25.txt

Output Set: N:\CRF3\10112001\I807470.raw

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3 <110> APPLICANT: TOHDOH, Naoki et al.
5 <120> TITLE OF INVENTION: NOVEL PROTEIN WAR-1 AND GENE THEREOF
7 <130> FILE REFERENCE: 0020-4850p
9 <140> CURRENT APPLICATION NUMBER: 09/807,470
10 <141> CURRENT FILING DATE: 2001-04-13
12 <160> NUMBER OF SEQ ID NOS: 13
14 <170> SOFTWARE: PatentIn version 3.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 2311
18 <212> TYPE: DNA
19 <213> ORGANISM: Rattus norvegicus
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (463)..(1554)
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27 gctccttaag ggaaggtgag attcctaaga gatcagtaga gagcaccagg gagctcgtcg      120
28 ctgtgttgct atggtgatga tggcaatggt aatgacagtg gcaccagatt tccctgttcc      180
29 tgggaagccc ctccggctcc cgcgggtggg cggcggcggc gatcgggtgcg gcaaaccgcg      240
30 gctcgcaccc gggcctgcgg ggcaggggcg cggcgctcga ttcccttccc tgcctctgca      300
31 gcccctgtgc gcatgctcgg cctacgcggc cccagccttt gattgatcgg tcggcagcgg      360
32 ctgcgaccct gggcggcaga cgggcgggga tggggagccc ggcgctggga gcggcgagc      420
33 gatcagcggg ggcggccggg gaggaccggg gaggaccgag gc atg ggg ctc cgc      474
34                                     Met Gly Leu Arg
35                                     1
36 aag aag aac gcc agg aac ccc ccg gtg ctg agc cac gaa ttc atg gtg      522
37 Lys Lys Asn Ala Arg Asn Pro Pro Val Leu Ser His Glu Phe Met Val
38 5      10      15      20
39 cag aac cac gcg gat atg gtc tcc tgc gtg ggc atg ttc ttc gtg ctg      570
40 Gln Asn His Ala Asp Met Val Ser Cys Val Gly Met Phe Phe Val Leu
41 25      30      35
42 gga ctt atg ttc gag ggc acg gcc gag atg tcg atc gtg ttc ctc acc      618
43 Gly Leu Met Phe Glu Gly Thr Ala Glu Met Ser Ile Val Phe Leu Thr
44 40      45      50
45 ctg cag cat gga gtc gtt gtc cca gcg gaa ggg cta ccc tcg ggg tcc      666
46 Leu Gln His Gly Val Val Val Pro Ala Glu Gly Leu Pro Ser Gly Ser
47 55      60      65
48 agg acc ctt tac cat tat ggg gtc aaa gat ctg gcc aca gtg ttc ttc      714
49 Arg Thr Leu Tyr His Tyr Gly Val Lys Asp Leu Ala Thr Val Phe Phe
50 70      75      80
51 tac atg ctg gtg gcc atc atc att cac gcc acc att cag gag tac gtg      762
52 Tyr Met Leu Val Ala Ile Ile Ile His Ala Thr Ile Gln Glu Tyr Val
53 85      90      95      100
54 cta gat aag ctc agc cgg aga ctg cag ctc acc aaa ggc aaa caa aac      810
55 Leu Asp Lys Leu Ser Arg Arg Leu Gln Leu Thr Lys Gly Lys Gln Asn
56 105      110      115
57 aaa ttg aat gag gcc ggg cag ctg agt gtg ttc tac ata gtg tct ggt      858

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73 Lys Leu Asn Glu Ala Gly Gln Leu Ser Val Phe Tyr Ile Val Ser Gly
74      120      125      130
76 atc tgg ggt atg atc att ctg gcc tct gag aac tgc ctg tca gac ccc      906
77 Ile Trp Gly Met Ile Ile Leu Ala Ser Glu Asn Cys Leu Ser Asp Pro
78      135      140      145
80 act cta ttg tgg aag tct cag ccc cac aac atg atg aca ttt cag atg      954
81 Thr Leu Leu Trp Lys Ser Gln Pro His Asn Met Met Thr Phe Gln Met
82      150      155      160
84 aaa ttt ttc tac atc tca cag ttg gct tac tgg ttt cat agt ttc ccg      1002
85 Lys Phe Phe Tyr Ile Ser Gln Leu Ala Tyr Trp Phe His Ser Phe Pro
86 165      170      175      180
88 gag ctc tac ttc cag aaa gtc agg aaa caa gat atc ccg ggt caa ctc      1050
89 Glu Leu Tyr Phe Gln Lys Val Arg Lys Gln Asp Ile Pro Gly Gln Leu
90      185      190      195
92 atc tac att ggc ctc cac ctc ttc cac att gga ggg gcc tat ctc ttg      1098
93 Ile Tyr Ile Gly Leu His Leu Phe His Ile Gly Gly Ala Tyr Leu Leu
94      200      205      210
96 tac ttg aac cac ctg ggc ctg ctg ctt ctg atg ctg cac tat gct gtc      1146
97 Tyr Leu Asn His Leu Gly Leu Leu Leu Leu Met Leu His Tyr Ala Val
98      215      220      225
100 gag ctc ctc tcc agc gtg tgc agc ctg ctt tac ttt ggg gat gag cgg      1194
101 Glu Leu Leu Ser Ser Val Cys Ser Leu Leu Tyr Phe Gly Asp Glu Arg
102      230      235      240
104 tac cag aaa ggg ttg tct ttg tgg cct atc gtg ttt ata tcc ggg aga      1242
105 Tyr Gln Lys Gly Leu Ser Leu Trp Pro Ile Val Phe Ile Ser Gly Arg
106 245      250      255      260
108 ctc gtg aca ctg att gtc tca gtg gtt aca gta ggg ctt cac ttg gcc      1290
109 Leu Val Thr Leu Ile Val Ser Val Val Thr Val Gly Leu His Leu Ala
110      265      270      275
112 ggg aca aat cgg aat gga aat gct ctc tct ggt aat gtc aat gtg ttg      1338
113 Gly Thr Asn Arg Asn Gly Asn Ala Leu Ser Gly Asn Val Asn Val Leu
114      280      285      290
116 gca gct aaa atc gct gtt ctg tcc tcg agt tgc agt atc cag gtg tac      1386
117 Ala Ala Lys Ile Ala Val Leu Ser Ser Ser Cys Ser Ile Gln Val Tyr
118      295      300      305
120 ata aca tgg acc ttg acg acc gtc tgg ctt cag aga tgg tta gaa gat      1434
121 Ile Thr Trp Thr Leu Thr Thr Val Trp Leu Gln Arg Trp Leu Glu Asp
122      310      315      320
124 gcg aat ctt cat gtc tgt ggg agg aag aga cgg tcc agg tcg aga aaa      1482
125 Ala Asn Leu His Val Cys Gly Arg Lys Arg Arg Ser Arg Ser Arg Lys
126 325      330      335      340
128 ggc aca gaa aat gga gtg gag aat cca aat aga ata gat tct cca cca      1530
129 Gly Thr Glu Asn Gly Val Glu Asn Pro Asn Arg Ile Asp Ser Pro Pro
130      345      350      355
132 aag aag aaa gag aaa gct cct tag cagttgcaag cgaattgatt cttacctcca      1584
133 Lys Lys Lys Glu Lys Ala Pro
134      360
136 agggaatcca cttcttctta tgttgtgtct ctgtgctaga gattttctgt tcttcagaac      1644
138 gggtcgtgct ttttgaatat tgctaataatg ttgtctaatag tgtttttaag gttttgcaga      1704

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140 cgtatgagtg ggggatgggg gttaagacta aaccaactcag cctctaaata cagtcagaat 1764
142 agttaacgga ccaacatctt atttagtttag gttcttacct caacgatttt ccaaacgttt 1824
144 tgtggtgatg actgcagaat tgtgtacata aataatagtt tctgtcttcc aatgttcttt 1884
146 atcgaattaa caagtctgct agcaaagtgg ttgttttctt caatgttctc ctgcaggata 1944
148 aagtggaaaa tctgataaag gttaaaactca aatcagtatt atgtaaccgt tgggattttt 2004
150 ttaaagtgtt ttaaattttac aatggaaagc atttgtcaaa ccaccaaaaa tatgtgttta 2064
152 attttatgag tagtaattgt tagtgcttac gccccatta aagcatcaaa atatgaatag 2124
154 atgacatgtg tggatgatatt gacatttagc gaatcaagat acctttaata aatatggtgg 2184
156 gttactaaag aagtaaacga cttcttctctg tttatttttaa acacttgtag aggaaaactc 2244
158 gcaaaattaa atattactga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2304
160 aaaaaaa 2311
163 <210> SEQ ID NO: 2
164 <211> LENGTH: 363
165 <212> TYPE: PRT
166 <213> ORGANISM: Rattus norvegicus
168 <400> SEQUENCE: 2
170 Met Gly Leu Arg Lys Lys Asn Ala Arg Asn Pro Pro Val Leu Ser His
171 1 5 10 15
174 Glu Phe Met Val Gln Asn His Ala Asp Met Val Ser Cys Val Gly Met
175 20 25 30
178 Phe Phe Val Leu Gly Leu Met Phe Glu Gly Thr Ala Glu Met Ser Ile
179 35 40 45
182 Val Phe Leu Thr Leu Gln His Gly Val Val Val Pro Ala Glu Gly Leu
183 50 55 60
186 Pro Ser Gly Ser Arg Thr Leu Tyr His Tyr Gly Val Lys Asp Leu Ala
187 65 70 75 80
190 Thr Val Phe Phe Tyr Met Leu Val Ala Ile Ile Ile His Ala Thr Ile
191 85 90 95
194 Gln Glu Tyr Val Leu Asp Lys Leu Ser Arg Arg Leu Gln Leu Thr Lys
195 100 105 110
198 Gly Lys Gln Asn Lys Leu Asn Glu Ala Gly Gln Leu Ser Val Phe Tyr
199 115 120 125
202 Ile Val Ser Gly Ile Trp Gly Met Ile Ile Leu Ala Ser Glu Asn Cys
203 130 135 140
206 Leu Ser Asp Pro Thr Leu Leu Trp Lys Ser Gln Pro His Asn Met Met
207 145 150 155 160
210 Thr Phe Gln Met Lys Phe Phe Tyr Ile Ser Gln Leu Ala Tyr Trp Phe
211 165 170 175
214 His Ser Phe Pro Glu Leu Tyr Phe Gln Lys Val Arg Lys Gln Asp Ile
215 180 185 190
218 Pro Gly Gln Leu Ile Tyr Ile Gly Leu His Leu Phe His Ile Gly Gly
219 195 200 205
222 Ala Tyr Leu Leu Tyr Leu Asn His Leu Gly Leu Leu Leu Leu Met Leu
223 210 215 220
226 His Tyr Ala Val Glu Leu Leu Ser Ser Val Cys Ser Leu Leu Tyr Phe
227 225 230 235 240
230 Gly Asp Glu Arg Tyr Gln Lys Gly Leu Ser Leu Trp Pro Ile Val Phe
231 245 250 255
234 Ile Ser Gly Arg Leu Val Thr Leu Ile Val Ser Val Val Thr Val Gly

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235          260          265          270
238 Leu His Leu Ala Gly Thr Asn Arg Asn Gly Asn Ala Leu Ser Gly Asn
239          275          280          285
242 Val Asn Val Leu Ala Ala Lys Ile Ala Val Leu Ser Ser Ser Cys Ser
243          290          295          300
246 Ile Gln Val Tyr Ile Thr Trp Thr Leu Thr Thr Val Trp Leu Gln Arg
247 305          310          315          320
250 Trp Leu Glu Asp Ala Asn Leu His Val Cys Gly Arg Lys Arg Arg Ser
251          325          330          335
254 Arg Ser Arg Lys Gly Thr Glu Asn Gly Val Glu Asn Pro Asn Arg Ile
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259          355          360
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263 <211> LENGTH: 2288
264 <212> TYPE: DNA
265 <213> ORGANISM: Homo sapiens
267 <220> FEATURE:
268 <221> NAME/KEY: CDS
269 <222> LOCATION: (477)..(1586)
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276 tactaatgaa gatgccacta aaaaaaagaa ttcaggagca tcttggcggt ggcagcgagt      180
278 ttgaagatgc gacgatcaac gttgaagatc accgctcgca accccggggc tggcgccggg      240
280 taggggcgcg gcgctcgatt tccttccctg cctccgcggt ccccttggtg cgcattgtca      300
282 gctcagctcg gccctcgact ttgatttatt tttttttotgg gggcgcgctg cgacccgga      360
284 ctgacttcgg gatgggaagt ggagcccccg gagctgctac cgtggcgggc gcgctgtgag      420
286 gagcagccag ggggaggcag ctgcggtctg ccggtgagta tccgggaagc gccacc atg      479
287                                     Met
288                                     1
290 ggg ctc cgt aag aag agc acc aag aac ccc ccc gtt ctc agc cag gaa      527
291 Gly Leu Arg Lys Lys Ser Thr Lys Asn Pro Pro Val Leu Ser Gln Glu
292          5          10          15
294 ttc atc ctg cag aat cat gcg gac atc gtc tcc tgc gtg ggg atg ttc      575
295 Phe Ile Leu Gln Asn His Ala Asp Ile Val Ser Cys Val Gly Met Phe
296          20          25          30
298 ttc ctg ctg ggg ctt gtg ttc gag gga aca gca gaa gca tcc atc gtg      623
299 Phe Leu Leu Gly Leu Val Phe Glu Gly Thr Ala Glu Ala Ser Ile Val
300          35          40          45
302 ttt ctc act ctt cag cac agt gtt gct gtc cct gca gca gag gaa caa      671
303 Phe Leu Thr Leu Gln His Ser Val Ala Val Pro Ala Ala Glu Glu Gln
304 50          55          60          65
306 gcc acg ggc tca aag tcc ctc tat tat tat ggt gtc aaa gat ttg gcc      719
307 Ala Thr Gly Ser Lys Ser Leu Tyr Tyr Tyr Gly Val Lys Asp Leu Ala
308          70          75          80
310 acg gtt ttc ttc tac atg ctg gtg gca atc att att cat gcc aca att      767
311 Thr Val Phe Phe Tyr Met Leu Val Ala Ile Ile Ile His Ala Thr Ile
312          85          90          95

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| | | |
|-----|---|------|
| 314 | cag gaa tat gtg ttg gat aaa att aac aag aga atg cag ttc acc aaa | 815 |
| 315 | Gln Glu Tyr Val Leu Asp Lys Ile Asn Lys Arg Met Gln Phe Thr Lys | |
| 316 | 100 105 110 | |
| 318 | gcg aaa caa aac aag ttt aac gag tct ggt cag ttt agt gtg ttc tac | 863 |
| 319 | Ala Lys Gln Asn Lys Phe Asn Glu Ser Gly Gln Phe Ser Val Phe Tyr | |
| 320 | 115 120 125 | |
| 322 | ttt ttt tct tgt att tgg ggc aca ttc att tta atc tct gaa aac tgc | 911 |
| 323 | Phe Phe Ser Cys Ile Trp Gly Thr Phe Ile Leu Ile Ser Glu Asn Cys | |
| 324 | 130 135 140 145 | |
| 326 | ctg tca gac cca act ctt ata tgg aag gct cgt ccc cat agc atg atg | 959 |
| 327 | Leu Ser Asp Pro Thr Leu Ile Trp Lys Ala Arg Pro His Ser Met Met | |
| 328 | 150 155 160 | |
| 330 | aca ttt caa atg aag ttt ttc tac ata tcc cag ttg gct tac tgg ttt | 1007 |
| 331 | Thr Phe Gln Met Lys Phe Phe Tyr Ile Ser Gln Leu Ala Tyr Trp Phe | |
| 332 | 165 170 175 | |
| 334 | cat gct ttt cct gaa ctc tac ttc cag aaa acc aaa caa gac atc | 1055 |
| 335 | His Ala Phe Pro Glu Leu Tyr Phe Gln Lys Thr Lys Lys Gln Asp Ile | |
| 336 | 180 185 190 | |
| 338 | cct cgt caa ctt gtc tac att ggt ctt cac ctc ttc cac att act gga | 1103 |
| 339 | Pro Arg Gln Leu Val Tyr Ile Gly Leu His Leu Phe His Ile Thr Gly | |
| 340 | 195 200 205 | |
| 342 | gct tat ctc ttg tac ttg aat cat ttg gga ctt ctt ctt ttg gta ctg | 1151 |
| 343 | Ala Tyr Leu Leu Tyr Leu Asn His Leu Gly Leu Leu Leu Leu Val Leu | |
| 344 | 210 215 220 225 | |
| 346 | cat tat ttt gtt gaa tta ctt tcc cac atg tgc ggc ctg ttt tac ttt | 1199 |
| 347 | His Tyr Phe Val Glu Leu Leu Ser His Met Cys Gly Leu Phe Tyr Phe | |
| 348 | 230 235 240 | |
| 350 | agt gat gaa aag tac cag aaa ggc ata tct ctg tgg gcc att gtg ttt | 1247 |
| 351 | Ser Asp Glu Lys Tyr Gln Lys Gly Ile Ser Leu Trp Ala Ile Val Phe | |
| 352 | 245 250 255 | |
| 354 | atc ttg ggt aga ctt gtg act tta att gtt tcc gta ctc act gtt ggg | 1295 |
| 355 | Ile Leu Gly Arg Leu Val Thr Leu Ile Val Ser Val Leu Thr Val Gly | |
| 356 | 260 265 270 | |
| 358 | ttt cac ctg gct gga tgc cag aat cgg aat cct gat gcc ctt act gga | 1343 |
| 359 | Phe His Leu Ala Gly Ser Gln Asn Arg Asn Pro Asp Ala Leu Thr Gly | |
| 360 | 275 280 285 | |
| 362 | aat gta aat gtg ttg gca gct aaa att gct gtt ctg tgc tcc agt tgc | 1391 |
| 363 | Asn Val Asn Val Leu Ala Ala Lys Ile Ala Val Leu Ser Ser Ser Cys | |
| 364 | 290 295 300 305 | |
| 366 | acg atc caa gcc tac gta aca tgg aac tta att act ctc tgg ctt cag | 1439 |
| 367 | Thr Ile Gln Ala Tyr Val Thr Trp Asn Leu Ile Thr Leu Trp Leu Gln | |
| 368 | 310 315 320 | |
| 370 | agg tgg gta gaa gat tct aat att cag gcc tca tgt atg aaa aag aaa | 1487 |
| 371 | Arg Trp Val Glu Asp Ser Asn Ile Gln Ala Ser Cys Met Lys Lys Lys | |
| 372 | 325 330 335 | |
| 374 | cgg tgc aga tct tct aaa aaa aga aca gaa aac gga gtg gga gtg gaa | 1535 |
| 375 | Arg Ser Arg Ser Ser Lys Lys Arg Thr Glu Asn Gly Val Gly Val Glu | |
| 376 | 340 345 350 | |
| 378 | act tca aat aga gta gac tgt ccg cca aag agg aaa gag aaa tct tca | 1583 |

VERIFICATION SUMMARY

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